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Om nucleic - nucleic search, using sw model

Run on: September 25, 2002, 06:26:33 ; Search time 2465.47 Seconds  
 (without alignments)  
 10991.764 Million cell updates/sec

Title: US-09-762-249-13

Perfect score: 1295

Sequence: 1 atccagcgccaggat.....aaaaaaaaaaaaaaaaaaa 1295

Scoring table: IDENTITY\_NUC

Gapext 1.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank:  
 1: gb\_ba: \*  
 2: gb\_htg: \*  
 3: gb\_in: \*  
 4: gb\_on: \*  
 5: gb\_ov: \*  
 6: gb\_pat: \*  
 7: gb\_ph: \*  
 8: gb\_pl: \*  
 9: qb\_pr: \*  
 10: qb\_ro: \*  
 11: qb\_ss: \*  
 12: qb\_sy: \*  
 13: qb\_un: \*  
 14: qb\_vl: \*  
 15: em\_ba: \*  
 16: em\_fun: \*  
 17: em\_in: \*  
 18: em\_in: \*  
 19: em\_mu: \*  
 20: em\_on: \*  
 21: em\_or: \*  
 22: em\_ov: \*  
 23: em\_pt: \*  
 24: em\_ph: \*  
 25: em\_pl: \*  
 26: em\_ro: \*  
 27: em\_sts: \*  
 28: em\_un: \*  
 29: em\_vl: \*  
 30: em\_htg\_hum: \*  
 31: em\_htg\_inv: \*  
 32: em\_htg\_other: \*  
 33: em\_htgo\_inv: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1284	99.2	1296	9 HSA012506
2	1226.4	94.7	104228	9 ALI35917
3	570.6	44.1	AF044309	AF044309 Homo sapi
4	453.4	35.0	1000	9 AF071504 Homo sapi
5	397.2	30.7	207379	AC031681 Mus muscu
6	374.4	28.9	864	9 AF038898 Homo sapi
7	209.2	16.2	240	9 HSA012501
8	135.6	10.5	156	11 G32023
9	125.4	9.7	825	10 RATSYNTX2B
10	124.8	9.6	486	6 AR11444
11	124.8	9.6	486	6 E127728 DNA encodin
12	124.8	9.6	564	6 AR111443 Sequence
13	124.8	9.6	564	6 E12727 DNA encodin
14	124.8	9.6	711	6 AR111442 Sequence
15	124.8	9.6	711	6 E12726 DNA encodin
16	124.8	9.6	798	6 AR111445 Sequence
17	124.8	9.6	867	6 E06630 DNA encodin
18	124.8	9.6	840	6 AR054307 Sequence
19	124.8	9.6	840	6 E06631 DNA encodin
20	124.8	9.6	840	6 E08288 DNA encodin
21	124.8	9.6	840	6 E192032 Sequence
22	124.8	9.6	867	6 AR054306 Sequence
23	124.8	9.6	867	6 E06630 DNA encodin
24	124.8	9.6	867	6 E08287 DNA encodin
25	124.8	9.6	867	6 E192031 Sequence
26	124.8	9.6	870	6 AR054305 Sequence
27	124.8	9.6	870	6 E08288 DNA encodin
28	124.8	9.6	2931	10 MUSDPIM Sequence
29	124.8	9.6	2940	6 AR054308 Sequence
30	124.8	9.6	2940	6 E06639 DNA encodin
31	124.8	9.6	2940	6 E08286 DNA encodin
32	124.8	9.6	2940	6 E192033 Sequence
33	122.6	9.5	870	10 RATSYNTX2C Sequence
34	121.6	9.4	911	6 177035 Sequence
35	121.6	9.4	911	10 RATSYNTX2A Sequence
36	118.4	9.1	2016	9 HSU12918 Human synta
37	118.4	9.1	2081	9 HUMRC1A Human synta
38	118.4	9.1	2088	9 HUMNS1A Human synta
39	117.2	9.1	790	6 177042 Sequence
40	117.2	9.1	2048	10 RATSSAP35K Sequence
41	117.2	9.1	2097	6 177033 Sequence
42	117.2	9.1	2097	10 RATSYNA Human synta
43	117.2	9.1	2130	9 RATTUS norvegicus
44	115.2	8.9	867	9 AF24771 Macaca mulatta
45	114.6	8.8	1175	9 HUMSYNTAXB Human mRNA

ALIGMENTS

RESULT 1

HSA012506 LOCUS HSA012506 DEFINITION Homo sapiens mRNA activated in tumor suppression, clone TSA21 extended.

ACCESSION AJ012506 VERSION AJ012506.1 GI:5441365 KEYWORDS tumor suppression.

SOURCE ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1296)  
 Authors: Roperech,J.P., Lehrlone,F., Prieur,S., Plouffe,L., Israeli,D., Tuynier,M., Neimani,M., Pasturaud,P., Gendron,M.C., Dausset,J., Oren,M., Amson,R.B. and Telerman,A.

TITLE SIAH-1 promotes apoptosis and tumor suppression through a network involving the regulation of protein folding, unfolding, and trafficking: identification of common effectors with p53 and

REFERENCE 2 (bases 1 to 1296)

Group: Further information can be found at  
<http://www.sanger.ac.uk/HTML/CRIC6>

RPL-83M4 is from the library RPCI-1 constructed by the group of  
 Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>

VECTOR: PCYPAC2

IMPORTANT: This sequence is not the entire insert of clone RPL-83M4  
 It may be shorter because we sequence overlapping sections only  
 once, except for a 100 base overlap.  
 The true left end of clone RPL-83M4 is at 1 in this sequence. The  
 true left end of clone R1-91J24 is at 104129 in this sequence.

## FEATURES

source	location/qualifiers
1..104228	/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="6" /clone="RPL-83M4" /clone_id="RPCI-1"
1302..1605	/note="AlusX repeat: matches 1..303 of consensus"
2223..2533	/note="L2 repeat: matches 1866..2190 of consensus"
2573..2617	/note="MIR repeat: matches 202..247 of consensus"
2581..2634	/note="L2 repeat: matches 2693..2747 of consensus"
2637..2861	/note="MIR repeat: matches 1..262 of consensus"
3966..4024	/note="AluY/FLAM repeat: matches 35..77 of consensus"
4613..4720	/note="27 copies 4 mer 92% conserved"
4759..5035	/note="AlusP repeat: matches 1..278 of consensus"
5613..5697	/note="MIR repeat: matches 65..150 of consensus"
5746..6018	/note="LTM16A repeat: matches 169..450 of consensus"
6681..6805	/note="MER5A repeat: matches 61..185 of consensus"
7197..7476	/note="2 copies 140 mer 85% conserved"
7544..7704	/note="L2 repeat: matches 2355..2530 of consensus"
7835..7962	/note="FLAMLC repeat: matches 2609..2746 of consensus"
8707..8977	/note="L2 repeat: matches 1..268 of consensus"
10041..10339	/note="AlusX repeat: matches 1..301 of consensus"
11563..12086	/note="FLAMLC repeat: matches 1..124 of consensus"
12102..12143	/note="AluY repeat: matches 98..142 of consensus"
12144..12456	/note="AlusX repeat: matches 1..304 of consensus"
12457..12617	/note="AlusO repeat: matches 142..282 of consensus"
12648..12786	/note="L2 repeat: matches 2595..2745 of consensus"
13356..13668	/note="AlusX repeat: matches 1..310 of consensus"
13845..14157	/note="AlusO repeat: matches 1..313 of consensus"
14484..14623	/note="MIR repeat: matches 70..212 of consensus"
15168..15497	/note="AlusX repeat: matches 1..311 of consensus"
15498..15557	/note="30 copies 2 mer cc 68% conserved"
15931..16276	/note="Trigger4(Zombi) repeat: matches 2383..2731 of consensus"

repeat\_region 16277..16587  
 /note="AluJB repeat: matches 6..312 of consensus"  
 16588..18382  
 /note="Trigger4(Zombi) repeat: matches 627..2383 of consensus"

repeat\_region 16997..17123  
 /note="Sequence from overlapping clone ba3B11 (AL512354). Assembly confirmed by restriction digest."

repeat\_region 18383..18643  
 /note="AluJO repeat: matches 7..275 of consensus"

repeat\_region 18644..19263  
 /note="Tigger4(Zombi) repeat: matches 1..527 of consensus"

repeat\_region 19527..19652  
 /note="MLTH repeat: matches 154..258 of consensus"

repeat\_region 20848..20937  
 /note="MIR repeat: matches 146..240 of consensus"

repeat\_region 20940..21242  
 /note="MLTH repeat: matches 70..429 of consensus"

repeat\_region 22808..23017  
 /note="MLTH repeat: matches 70..284 of consensus"

repeat\_region 23035..23336  
 /note="AluJB repeat: matches 1..309 of consensus"

repeat\_region 23523..23658  
 /note="AluJB repeat: matches 1..139 of consensus"

repeat\_region 23659..23917  
 /note="AluJB repeat: matches 21..285 of consensus"

repeat\_region 24084..24278  
 /note="AlusX repeat: matches 1..195 of consensus"

repeat\_region 25005..25087  
 /note="MIR repeat: matches 92..185 of consensus"

repeat\_region 26139..26440  
 /note="AlusG repeat: matches 1..299 of consensus"

repeat\_region 26889..27041  
 /note="MIR repeat: matches 78..252 of consensus"

repeat\_region 27623..28017  
 /note="MER5A repeat: matches 1..364 of consensus"

repeat\_region 29032..29383  
 /note="AlusX repeat: matches 1..354 of consensus"

repeat\_region 29985..30289  
 /note="AlusX repeat: matches 1..307 of consensus"

repeat\_region 3013..30457  
 /note="MER5A repeat: matches 2..189 of consensus"

repeat\_region 32411..33100  
 /note="LPA7 repeat: matches 5426..6134 of consensus"

repeat\_region 33301..33342  
 /note="MIR repeat: matches 71..232 of consensus"

repeat\_region 34707..34752  
 /note="MER5A repeat: matches 2..189 of consensus"

repeat\_region 34819..34990  
 /note="LIP5 repeat: matches 5972..6143 of consensus"

repeat\_region 34992..35031  
 /note="10 copies 4 mer aaat 85% conserved"

misc\_feature 35362..36323  
 /note="CpG island"

repeat\_region 37387..37697  
 /note="not experimental

repeat\_region 37710..37993  
 /note="AluY repeat: matches 1..311 of consensus"

repeat\_region 38849..39089  
 /note="AluO repeat: matches 1..286 of consensus"

repeat\_region 40658..40945  
 /note="MIR repeat: matches 2..262 of consensus"

repeat\_region 41221..41256  
 /note="AlusX repeat: matches 1..288 of consensus"

repeat\_region 41267..41347  
 /note="18 copies 2 mer ac 100% conserved"

repeat\_region 41323..41464  
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repeat\_region 41487..41557  
 /note="L2 repeat: matches 2007..2143 of consensus"

repeat\_region 41558..41965  
 /note="LIMB2 repeat: matches 6099..6167 of consensus"

/note="MSIA repeat: matches 1..426 of consensus"

		TITLE		Syntaxin 11 is a novel SNARE protein associated with the trans-Golgi network and late endosomes	
		JOURNAL		Unpublished	
		REFERENCE		2 (bases 1 to 1000)	
AUTHORS		Valdez,A.C., Cabaniols,J.-P., Brown,M.J. and Roche,P.A.		TITLE	
JOURNAL		Submitted (10-JUN-1998) NCI/EIB, NIH, 10 Center Drive, Bethesda, MD		20892, USA	
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		source		Location/Qualifiers	
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		/tissue_type="placenta"		/tissue_type="placenta"	
		55..918		/note="SNARE protein"	
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		/db_xref="GI:3241240"		/db_xref="GI:3241240"	
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		BASE COUNT		ORIGIN	
		224		TLCCFCPCPLK*	
		Query Match		CDS	
		44.1% ; Score 570.6; DB 9; Length 1280;		55..918	
Best Local Similarity		Matches 606; Conservative 0; Mismatches 4; Indels 3; Gaps 3;		/note="SNARE protein"	
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Db		664 ATCCAGGCCACCTGGATCATGGGAAGGGAGTCCTGGGGACAGATCGAGCATG 723		/protein_id="AAC24041"	
Qy		61 ttccgacgggttaagtggacgtttccggacgttgccggacgtggacgtggacgtggcg 120		/db_xref="GI:3241240"	
Db		724 TTCCGAGCAGGGTAAGTGGACCTGTTCCGAGAACTGTGCTGGCCGAGTGAAGGC-CG 782		/translation="MKDLAELLDLSKQDQPGDFDEFSPHEDIVFETDILESLYRDIRQIDEQNLVADVKRKGQNARFLTSKRLSSIKRDTNSTAKAFRGEVICLKRAMKELSEAAEQAQPHSAVARISRAOYALTLTQFRAHIDYNAEMKORDNCKIRIQRQLEMGKVSYSGQDOEDMFSOKWQDQGKARALNEESRLRLESIQRDVBELFLQMVAVLEVKOQDINTLNENVOKTVDTGQAKAQVRAYOERKPER	
Qy		121 cggccgccttcacagatcgaggatcgaggacggccggactctcgccgtggagacgg- 179		/translation="MKDLAELLDLSKQDQPGDFDEFSPHEDIVFETDILESLYRDIRQIDEQNLVADVKRKGQNARFLTSKRLSSIKRDTNSTAKAFRGEVICLKRAMKELSEAAEQAQPHSAVARISRAOYALTLTQFRAHIDYNAEMKORDNCKIRIQRQLEMGKVSYSGQDOEDMFSOKWQDQGKARALNEESRLRLESIQRDVBELFLQMVAVLEVKOQDINTLNENVOKTVDTGQAKAQVRAYOERKPER	
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Db		843 CTCCCGCACGTACAGCAGCTTCTGCACTGGCCG 902		/protein_id="AAC24041"	
Qy		240 caccctgaaacctcgatcgaggatcgacgttccggacgttccggacggcc 299		/db_xref="GI:3241240"	
Db		903 CACCCCTGAACGCCATCGAGCTACAGTACAAAGACGGTCGACTACACGGCCAGGCCAA 962		/translation="MKDLAELLDLSKQDQPGDFDEFSPHEDIVFETDILESLYRDIRQIDEQNLVADVKRKGQNARFLTSKRLSSIKRDTNSTAKAFRGEVICLKRAMKELSEAAEQAQPHSAVARISRAOYALTLTQFRAHIDYNAEMKORDNCKIRIQRQLEMGKVSYSGQDOEDMFSOKWQDQGKARALNEESRLRLESIQRDVBELFLQMVAVLEVKOQDINTLNENVOKTVDTGQAKAQVRAYOERKPER	
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Qy		360 ctctcggtgtccgtgtccgtatcgaggatcgaggatcgaggatcgaggatcg 419		/product="syntaxin 11"	
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Qy		420 catggagcgccgtggaaaggccgttccggacgttccggatcgaggatcg 479		/db_xref="GI:3241240"	
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Qy		480 cccaaaccttcggactcggttttagaaaaaaaacggccgttcaagatcg 539		/translation="MKDLAELLDLSKQDQPGDFDEFSPHEDIVFETDILESLYRDIRQIDEQNLVADVKRKGQNARFLTSKRLSSIKRDTNSTAKAFRGEVICLKRAMKELSEAAEQAQPHSAVARISRAOYALTLTQFRAHIDYNAEMKORDNCKIRIQRQLEMGKVSYSGQDOEDMFSOKWQDQGKARALNEESRLRLESIQRDVBELFLQMVAVLEVKOQDINTLNENVOKTVDTGQAKAQVRAYOERKPER	
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AF071504		LCUS AF071504 Homo sapiens		/note="SNARE protein"	
DEFINITION		Homo sapiens syntaxin 11 mRNA, complete cds.		/note="SNARE protein"	
VERSION		AF071504.1		/note="SNARE protein"	
KEYWORDS		human.		/note="SNARE protein"	
ORGANISM		Homo sapiens		/note="SNARE protein"	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. 1 (bases 1 to 1000).		/note="SNARE protein"	
AUTHORS		Valdez,A.C., Cabaniols,J.-P., Brown,M.J. and Roche,P.A.		/note="SNARE protein"	
SOURCE		human.		/note="SNARE protein"	
RESULT		5		/note="SNARE protein"	
AC091681		LOCUS AC091681		/note="SNARE protein"	
DEFINITION		Mus musculus chromosome 10 clone rp23-111d4 strain C57BL/6J,		/note="SNARE protein"	
ACCESSION		WORKING DRAFT SEQUENCE, 29 unordered pieces.		/note="SNARE protein"	
VERSION		AC091681		AC091681.27	
		GI:18390231		GI:18390231	



Db	448	ATCCAGGGCAGCTAGAGTACGGAGAACCACTGACGAGAGCTGAGAGATG	507
Oy	61	tccgagcaggtagtggagcttttcgagaacttgtggccacggcgactgtggccatgtggaaaggcg	120
Db	508	CTGGAGAGGGAGCCGCCATCTCATCTCGGACATTATCAGATTCAGAGTACT	567
Oy	121	cggccccctcacgaaatcgggagccacccggcactgtggccatgtggccatgtggaaaggcg	180
Db	568	AGCAAGCTCTCATGTAGATGAGTCACGCCAACAGACATCATGAGCAGACAG	627
Oy	181	atccgcacgtacacgaaacttttgcgatgcgggtgtggagaaaggcggccatgtggaaaggcg	240
Db	628	ATCCGAGACTGCACGAGTGTTCATGGATATGCCATGTTGAGACTCAGGTGAA	687
Oy	241	acctgacgtcatcgacgtcaacgtacaaaggccgttgcgtactacccggcaggcca	300
Db	688	ATGGTCACACACATGTAGAGAACGTGGACTCGTAGATTACGTGAGCACGCCAG	747
Oy	301	gcccgggtggggaggccgtggatcgaggagaaacccgtccggaccctgtgc	360
Db	748	GAGAGACTAAGAACCTACAATAACAGAGCAAGGCCAGGGTGCTCTGCT	807
Oy	361	ttctgtgtttccctgc	375
Db	808	CTGGCCGACAGTGC	822
RESULT 10			
LOCUS	AR11444	AR11444	
DEFINITION	Sequence 13 from patent US 6127149.	486 bp	DNA
ACCESSION	AR11444.1	GI:12828292	
KEYWORDS	;		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 486)		
AUTHORS	Hirai,Y., Koshida,S. and Oka,Y.		
VERSION			
JOURNAL	Modified epimorphin		
FEATURES	Patent: US 6127149-A 13-03-OCT-2000; Location/Qualifiers		
source	1. .486 /organism="unknown"		
BASE COUNT	152 a	110 c	139 g
ORIGIN			85 t
very Match 9.6%; Score 124 8; DB 6; Length 486; ast Local Similarity 60.7%; Pred. No. 3.9e-10; Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;			
Query Match 9.6%; Score 124 8; DB 6; Length 486; Best local similarity 60.7%; Pred. No. 3.9e-10; Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;			
Qy	1	atccagegcacgtggatcatggggcaaggaaactctccggcaccatcgaggatcg	60
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Oy	61	tccgagcaggtagtggagcttttcgagaacttttgcgatcgaggaaaggccg	120
Db	193	CTGGAGAGGGAGCCCTCCATCTCGGATATTATCATGATCACAAATCCT	252
Oy	121	cgggccgcctcaacggatcgaggccgcacccggcactgtggccatgtggaaaggcg	180
Db	253	AGGAAGCTCTCATGTAGAGATCGAGTCGAGGCCAACAGACATCGAGTGAGACAG	312
Oy	181	atccgcacgtacacgaaacttttgcgatgcgggtctgtggagaaaggccgcac	240
Db	313	ATCCGAGACTGCACGAGATGTCATGGATATGCCATGTTGAGACTCAGGTGAA	372
Oy	241	acctgacgtcatcgacgtcaacgtacaaaggccgttgcgtactacccggcaggca	300
Db	373	ATGGTCACACATCGAGAGAAATGTCGAGACTCTGTGAGATTACGTGAGACATCGAG	432
Oy	301	gcccgggtggggaggccgtggatcgaggagaaacccgtccggaccctgtgc	360
Db	433	GAAGAGCAGAGAACCATCAATCCAGAGCAAG	468
RESULT 11			
Locus	E12728	486 bp	DNA
DEFINITION	DNA encoding mouse Epmorphin-derived peptide.		
VERSION	E12728		
KEYWORDS	;		
ORGANISM	unidentified		
REFERENCE	1 (bases 1 to 486)		
AUTHORS	Koshida,S., Oka,Y. and Hirai,Y.		
TITLE	TAILORED DERIVATIVE OF EPMORPHIN		
JOURNAL	Patent: JP 199705885-A/7 11-MAR-1997;		
COMMENT	SUMITOMO ELECTRIC IND LTD		
OS	None		
OC	Artificial sequences.		
PN	JP 199705885-A/7		
PD	11-MAR-1997		
PR	29-MAR-1996 JP 1996099584		
KOSHIDA SHOZO, OKA YUMIKO, HIRAI YOHEI	99980, 19-JUN-1995 JP 95P	175540	PI
PC	C12N15/09, C07H21/04, C07K7/06, C07K7/08, C07K14/485, PC		
CPC	(C12P21/02/A61K39/00, C12P21/02/C12R1/19);		
CC	strandedness: Double;		
CC	topology: Linear; Location/Qualifiers		
FH	Key		
FT	source		
FT	1. .485 /organism="Artificial sequences"		
FT	mat_peptide		
FT	(23) /product="Epmorphin fragment designated		
FT	FT		
FT	/note= fragment (23) is derived from 104-264		
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source	1. .486 /organism="unidentified"		
BASE COUNT	152 a	110 c	139 g
ORIGIN			85 t
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Qy	1	atccagcaggtagtggatcatggggcaaggaaacttttgcgatcgaggaaaggccg	60
Db	133	ATCCAGGCCAGCTGGAGATCCTGGGGAGGACCACTGACGAGAGCTGGAGATG	192
Oy	61	tccgagcaggtagtggagcttttcgagaacttttgcgatcgaggaaaggccg	120
Db	193	CTGGAGAGGGAGCCCTCCATCTCGGATATTATCATGATCACAAATCCT	252
Oy	121	cgggccgcctcaacggatcgaggccgcacccggcactgtggccatgtggaaaggcg	180
Db	253	AGGAAGCTCTCATGTAGAGATCGAGTCGAGGCCAACAGACATCGAGTGAGACAG	312
Oy	181	atccgcacgtacacgaaacttttgcgatgcgggtctgtggagaaaggccgcac	240
Db	313	ATCCGAGACTGCACGAGATGTCATGGATATGCCATGTTGAGACTCAGGTGAA	372
Oy	241	acctgacgtcatcgacgtcaacgtacaaaggccgttgcgtactacccggcaggca	300
Db	373	ATGGTCACACATCGAGAGAAATGTCGAGACTCTGTGAGATTACGTGAGACATCGAG	432
Oy	301	gcccgggtggggaggccgtggatcgaggagaaacccgtccggaccctgtgc	360

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Best Local Similarity	60.7%	Pred. No. 4.2e-10;		Mismatches 0;
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Author	1	atccaggccactggagatcatggcaaggaaatctcggggaccatcgaggacat	60	
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Keywords	ATCCAGCGCAGCTGGAGATCACTGGGAGACCACACTGAGCTGGAGAGAT	417		
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Reference	1			
Locus	E12726	atccggaggactacaggcttcttcggatggggatgtttcccgagaacttgtcgccac	60	
Definition	DNA encoding mouse Epimorphin-derived peptide.	ttcggaggaggtaatggggactgtttcccgagaacttgtcgccacatcgaaatcgat	60	
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Journal	JP 199705885;A/5.	ttcggaggaggtaatggggactgtttcccgagaacttgtcgccacatcgaaatcgat	60	
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Event	None	ttcggaggaggtaatggggactgtttcccgagaacttgtcgccacatcgaaatcgat	60	
Reference	1	(bases 1 to 711)		
Author	Koshida,S., Oka,I. and Hirai,Y.			
Title	TAILORED DERIVATIVE OF EPIMORPHIN			
Journal	JP 199705885-A 5 11-MAR-1997;			
Sumitomo Electric Ind Ltd				
OS	None			
OC	Artificial sequences.			
PN	JP 199705885			
PD	11-MAR-1997			
PF				
PR	31-MAR-1995 JP 95P 99980, 19-JUN-1995 JP 95P 175540 PI			
PC	KOSHIDA, SHOGO, OKA, YUMIKO, HIRAI, YOHJI			
C1	C12N15/09, C0H21/04, C07K7/06, C07K7/08, C07K14/485, PC			
CC	(C12P21/02, A61K38/00, C12R1/19);			
Strandedness:	Double;			
CC	topology: Linear;			
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Features	Location/Qualifiers	1. .711		

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## On nucleic - nucleic search, using sw model

Run on:

September 24, 2002, 14:13:36 ; Search time 237.5 seconds

(without alignments)

9361.702 Million cell updates/sec

## Title:

US-09-762-249-13

Perfect score:  
Sequence:

1 atccageggcaggat.....aaaaaaaaaaaaaaa 1295

## Scoring table:

IDENTITY.NUC  
Gapop 10.0 , Gapext 1.0Searched:  
Maximum DB seq length: 1736436 seqs, 858457221 residuesPost-processing:  
Minimum Match 0%

Maximum Match 100%

Total number of hits satisfying chosen parameters:  
Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Listing first 45 summaries

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## RESULT

1 AA261485 ID AA261486 standard; cDNA; 240 BP.

XX AC AA261486;

XX DT 19-JUN-2000 (first entry)

XX DE cDNA sequence of tumour suppressor activated pathway gene TSAP21.

XX KW Tumour suppressor activated pathway gene; TSAP; apoptosis;

KW tumour suppression; tumour suppressor inhibited pathway gene; TSIP3;

KW cancer; antiviral; ss.

OS Homo sapiens.

XX PN FR2782085-A1.

XX PD 11-FEB-2000.

XX PF 05-AUG-1998; 98FR-0010077.

XX PR 05-AUG-1998; 98FR-0010077.

XX PA (DAUS-) FOND DAUSSET-CEPH JEAN.

XX PT Ansor R, Telerman A;

XX DR WP1; 2000-208788/19.

XX PT Nucleic acid sequences correspond to genes whose expression is induced or inhibited

PT Inflections corresponds to genes whose expression is induced or inhibited

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	209.2	16.2	240 21 AAZ61486	cDNA sequence of t
2	124.8	9.6	486 17 AAT16088	Mouse epimorphin f
3	124.8	9.6	486 18 AAT6243	Mouse epimorphin f
4	124.8	9.6	564 17 AAT16087	Mouse epimorphin f
5	124.8	9.6	564 18 AAT6212	Mouse epimorphin f
6	124.8	9.6	711 17 AAT16086	Mouse epimorphin f
7	124.8	9.6	711 18 AAT6241	Mouse epimorphin f
8	124.8	9.6	798 17 AAT16090	Mouse epimorphin f
9	9.6	7.98	18 AAT62414	Mouse epimorphin C

Result No.	Score	Query Match Length	DB ID	Description
1	209.2	16.2	240 21 AAZ61486	cDNA sequence of t
2	124.8	9.6	486 17 AAT16088	Mouse epimorphin f
3	124.8	9.6	486 18 AAT6243	Mouse epimorphin f
4	124.8	9.6	564 17 AAT16087	Mouse epimorphin f
5	124.8	9.6	564 18 AAT6212	Mouse epimorphin f
6	124.8	9.6	711 17 AAT16086	Mouse epimorphin f
7	124.8	9.6	711 18 AAT6241	Mouse epimorphin f
8	124.8	9.6	798 17 AAT16090	Mouse epimorphin f
9	9.6	7.98	18 AAT62414	Mouse epimorphin C









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OM nucleic - nucleic search, using sw model  
Run on: September 24, 2002, 14:12:02 ; Search time 66.07 seconds

Title: 4814\_521 Million cell update!  
 Perfect score: US-09-762-249-13  
 Sequence: 1235  
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 Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues  
Total number of hits satisfying chosen parameters

卷之三

ALIGNMENT

#### Post-processing: Minimum Match 0%

Listing first 45 summaries

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4: /cgn2_6/ptodata/2/1na/6B_COMB.seq: *
5: /cgn2_6/ptodata/2/1na/PCNTUS_COMB.seq: *
6: /cgn2_6/ptodata/2/1na/backfiles1.sec

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score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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No. Score Match Length DB ID

134 8 9 6 186 3 116

卷之三

14  
124.  
.8  
9.  
.6  
798  
.3  
US

- 6 124.8 9.6 840 2 US

8 124.8 9.6 867 2 US

10 124.8 9.6 870 2 US

12 124.8 9.6 2940 2 US

14 117.2 9.1 790 US

13 117.2  
16 107.3  
1 8.3  
1300 1  
ITS 0.3

18 1/10/2  
94 4 7.8  
486 3000 US  
WT 155

19  
94.4  
7.3  
364  
US

21 94.4  
22 7.3  
23 795  
24 3  
25 831  
26 1  
27 1

23 94.4 7.3 834 2 US

25 94.4 7.3 864 2 US

26 94.4 7.3 867 1 US

27 94.4 7.3 867 2 US

RESULT 4  
US-08-493-071-14  
; Sequence 14, Application US/08493071  
; Patent No. 6127149

GENERAL INFORMATION:  
 APPLICANT: Hirai, Yohei  
 APPLICANT: Koshida, Shogo  
 APPLICANT: Oka, Yumiko  
 TITLE OF INVENTION: MODIFIED EPIMORPHIN  
 NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: LOVE, PRICE, LEBLANC & BECKER  
 STREET: 99 CANAL CENTER PLAZA, SUITE 300  
 CITY: ALEXANDRIA  
 STATE: VA  
 COUNTRY: USA  
 ZIP: 22314

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/493,071  
 FILING DATE: 1996-08-08  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Price, Robert L.  
 REGISTRATION NUMBER: 22,685  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 703-684-1124

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 798 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-493-071-14

Query Match 9.6%; Score 124.8; DB 3; Length 798;  
 Best Local Similarity 60.7%; Pred. No. 6.1e-19; Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

RESULT 5  
US-08-690-457-14  
; Sequence 14, Application US/08690457  
; Patent No. 572698

GENERAL INFORMATION:  
 APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.  
 TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE  
 TITLE OF INVENTION: DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTI-TUMOR AGENTS  
 NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA,  
 ADDRESS: Japan  
 STREET: 1, Taya-cho  
 CITY: Yokohama-shi  
 COUNTRY: Japan  
 ZIP: 244

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/690,457  
 FILING DATE: 16-AUG-1996  
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/078,309  
 FILING DATE: June 15, 1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 294856/1991  
 FILING DATE: October 16, 1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 122206/1992  
 FILING DATE: April 17, 1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 135592/1992  
 FILING DATE: April 30, 1992

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:  
 LENGTH: 840  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-690-457-14

Query Match 9.6%; Score 124.8; DB 1; Length 840;  
 Best Local Similarity 60.7%; Pred. No. 6.2e-19; Matches 204; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

MOLECULE TYPE: cDNA  
US-08-690-457-13

Query Match 9.6%; Score 124.8; DB 1; Length 867;

Best Local Similarity 60.7%; Pred. No. 6.3e-19; Mismatches 132; Indels 0; Gaps 0;

Matches 204; Conservative 0; MisMatches 132; Indels 0; Gaps 0;

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Qy 61 ttccgacggggaaatggggactgttttccggaaactgtggggccgg 120  
Db 505 CTGGAGAGGGAAAGCCGCATCTCATCGATATTATCAGATTCACAATCACT 564

Qy 121 cggcccccttaacgagatcgagccacccgcgaactgtgcgtggag 180  
Db 565 AGCGAACCTCTCATGAGATCGAGTCCGCCAACAGACATCAGAAGCTGGAGACAGC 624

Qy 241 accctggacgttcacgggtttttccggatgggggtgggggggggg 300  
Db 685 ATGGTCACAACATCGAGAGATGTGGTCACTCTGAGATTTACGTGGAACATGCCAG 744

Qy 301 ggcgcagggtcgccggaggccgtggatcgaggaaatgggggg 336  
Db 745 GAAGAGACGAAGAACCATCACATACCGAGCAAG 780

RESULT 8

US-08-628-187-13  
Sequence 13, Application US/08628187

Patent No. 5837239

PATENT INFORMATION:

APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.  
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED

NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan  
STREET: 1, Taya-cho  
CITY: Yokohama-shi  
COUNTRY: Japan  
ZIP: 244

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patientin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/628,187  
FILING DATE: April 5, 1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 294856/1991  
FILING DATE: October 16, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 294857/1991  
FILING DATE: October 16, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 122906/1992  
FILING DATE: April 17, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 135692/1992  
FILING DATE: April 30, 1992  
SEQUENCE CHARACTERISTICS:  
LENGTH: 867  
TYPE: nucleic acid

STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-628-187-13  
MOLECULE TYPE: cDNA

Query Match 9.6%; Score 124.8; DB 2; Length 867;

Best Local Similarity 60.7%; Pred. No. 6.3e-19; Mismatches 132; Indels 0; Gaps 0;

Matches 204; Conservative 0; MisMatches 132; Indels 0; Gaps 0;

Qy 1 atccagcggcaactggggactgttttccggaaactgtggggccgg 120  
Db 445 ATCCAGGCCACTGGAGATCCTGGGGACCCACTGACCGAGCTGAGAGATG 504

Qy 61 ttccgacggggaaatggggactgttttccggaaactgtggggccgg 120  
Db 505 CTGGAGAGGGAAAGCCGCATCTCATCGATATTATCAGATTCACAATCACT 564

Qy 121 cggcccccttaacgagatcgagccacccgcgaactgtgcgtggag 180  
Db 565 AGCGAACCTCTCATGAGATCGAGTCCGCCAACAGACATCAGAAGCTGGAGACAGC 624

Qy 241 accctggacgttcacgggtttttccggatgggggtgggggggg 300  
Db 685 ATGGTCACAACATCGAGAGATGTGGTCACTCTGAGATTTACGTGGAACATGCCAG 744

Qy 301 ggcgcagggtcgccggaggccgtggatcgaggaaatgggggg 336  
Db 745 GAAGAGACGAAGAACCATCACATACCGAGCAAG 780

RESULT 9

US-08-690-457-12  
Sequence 12, Application US/08690457

Patent No. 5726298

PATENT INFORMATION:

APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.  
TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND AN

NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan  
STREET: 1, Taya-cho  
CITY: Yokohama-shi  
COUNTRY: Japan  
ZIP: 244

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patientin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/690,457  
FILING DATE: 16-AUG-1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/078,309  
FILING DATE: June 15, 1993  
APPLICATION NUMBER: 29885/1991  
FILING DATE: October 16, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 294857/1991  
FILING DATE: October 16, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 122906/1992  
FILING DATE: April 17, 1991  
PRIOR APPLICATION DATA:

FILING DATE: October 16, 1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 294857/1991  
FILING DATE: October 16, 1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 122906/1992  
FILING DATE: April 17, 1991  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 135692/1992  
FILING DATE: April 30, 1992  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2940  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 294855/1991  
FILING DATE: October 16, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 294857/1991  
FILING DATE: October 16, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 122905/1991  
FILING DATE: April 17, 1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 135692/1991  
FILING DATE: April 30, 1992

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 2940  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

Query Match 9.6%; Score 124.8; DB 1; Length 2940;  
 Best Local Similarity 60.7%; Pred. No. 1.1e-18;  
 Matches 204; Conservative 0; Mismatches 132; Indels 0; gaps 0;

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 Db 657 CTGGAGAGGGAGGCCATCATCGATCGGATATATCGAGATCACAAATCACT 716  
 Qy 121 cggccgcctcaacgagatcgccacccgcgactgtcgccgtggagggccgc 180  
 Db 717 AGGCAAGCTCTCAATGAGATCGAGTCCCACAAAGAACATCATGAGCTGGAGACCG 776  
 Qy 181 atccgcgcgtacacgagtttcgtcgatgggggtgtggagacggccac 240  
 Db 777 ATCCGAGACTGCAGGATGTCATGGATGGCATGTTGTGAGACAGGTGA 836  
 Qy 241 accctgaaggatcgacgatcaacaaagacggctactacccggccacggca 300  
 Db 837 ATGGTCACAACATCGAGGAAATCTGGCACTCTGTAGATTACGTGGACATGCCAAG 896  
 Qy 301 gcgcaggatcgagggccgtcagtgaggaaag 336  
 Db 897 GAAGAGACAAAGGCCATCAATACCAAGAGCAAG 932

ULT 12  
 08-628-187-15  
 Sequence 15, Application US/08628187  
 ;  
 PATENT NO. 5837239  
 GENERAL INFORMATION:  
 APPLICANT: BIOMATERIAL RESEARCH INSTITUTE CO., LTD.  
 TITLE OF INVENTION: NOVEL PHYSIOLOGICALLY ACTIVE SUBSTANCE DESIGNATED AS EPIMORPHIN, GENES ENCODING THE SAME, AND ANTIBODIES THERETIC NUMBER OF SEQUENCES: 15  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: 1, Taya-cho, Sakae-ku, Yokohama-shi, KANAGAWA, Japan  
 STREET: 1, Taya-cho  
 CITY: Yokohama-shi  
 COUNTRY: Japan  
 ZIP: 244  
 COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08628, 187  
 FILING DATE: April 5, 1996  
 CLASSIFICATION: 435

Query Match 9.6%; Score 124.8; DB 2;  
 Best Local Similarity 60.7%; Pred. No. 1.1e-18;  
 Matches 204; Conservative 0; Mismatches 132; Indels 0; gaps 0;

Qy 1 atccaggcgcacgtggadatcatcgatggcaaggaaactcgccg 60  
 Db 597 ATCCAGCGCAGCTGGAGATCACTGGAGACCACTGAGCTGGAGATG 656  
 Qy 61 ttcgagcgggtatgtggactgtttcgagaacttgcggcggactgtggcg 120  
 Db 657 CTGGAGAGGGAGGCCATCATCGATCGGATATATCGAGATCACAAATCACT 716  
 Qy 121 cggccgcctcaacgagatcgccacccgcgactgtcgccgtggagggccgc 180  
 Db 777 ATCCGAGACTGCAGGATGTCATGGATGGCATGTTGTGAGACAGGTGA 836  
 Qy 241 accctgaaggatcgacgatcaacaaagacggctactacccggccacggca 300  
 Db 837 ATGGTCACAACATCGAGGAAATCTGGCACTCTGTAGATTACGTGGACATGCCAAG 896  
 Qy 301 gcgcaggatcgagggccgtcagtgaggaaag 336  
 Db 897 GAAGAGACAAAGGCCATCAATACCAAGAGCAAG 932

RESULT 13  
 US-08-393-985-5  
 Sequence 5, Application US/08393985  
 ;  
 PATENT NO. 5693476  
 GENERAL INFORMATION:  
 APPLICANT: Scheller, Richard H.  
 TITLE OF INVENTION: Methods and Compositions for Treatment of Vesicular Release of Sequences: 35  
 NUMBER OF SEQUENCES: 35  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Dehlinger & Associates  
 STREET: 350 Cambridge Avenue, Suite 250  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94306  
 COMPUTER READABLE FORM:  
 COMPUTER: Floppy disk  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08628, 187  
 FILING DATE: April 5, 1996  
 CLASSIFICATION: 435



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OM nucleic - nucleic search, using sw model

Run on: September 24, 2002, 12:53:01 ; Search time 1809.41 Seconds  
(without alignments)  
9659.810 Million cell updates/sec

Title:	US-09-762-249-13
Perfect score:	1225
Scoring table:	IDENTITY_NUC GapP 10.0 , Gapext 1.0
Searched:	13736207 seqs, 678477542 residues
Total number of hits satisfying chosen parameters:	27472414
Minimum DB seq length:	0
Maximum DB seq length:	200000000
Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

Database : EST:  
1: em\_estba: \*  
2: em\_easthum: \*  
3: em\_estin: \*  
4: em\_estmu: \*  
5: em\_estpl: \*  
6: em\_estro: \*  
8: em\_htc: \*  
9: gb\_est1: \*  
10: gb\_est2: \*  
11: gb\_htc: \*  
12: gb\_gss: \*  
13: em\_gss\_hum: \*  
14: em\_gss\_inv: \*  
15: em\_gss\_pn: \*  
16: em\_gss\_virt: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	728	562	739	10 BI518995
C. 2	658.6	50.9	911	10 BI519330
C. 3	543.2	41.9	571	10 BM149227
C. 4	521.0	40.2	598	10 BF892936
C. 5	487.4	37.6	525	10 BF894780
C. 6	465.4	35.9	525	10 BF892927
C. 7	456.4	35.9	480	10 BF15864
C. 8	447.8	34.6	470	9 AJ275149
C. 9	439.8	34.0	464	10 BF893339
C. 10	429.6	34.2	9 AW026277	rw11a05.x
C. 11	421.4	32.5	434	9 AA227632
C. 12	416.4	32.2	499	9 AW500047
C. 13	411.1	429	9 BF893543	OY1-MT013
C. 14	402.4	31.1	426	9 AA262151
C. 15	397.2	30.7	2219	11 AK017897
C. 16	393.4	30.4	406	9 AW662909
C. 17	384.7	29.7	409	9 AW500048

ALIGMENTS

RESULT	1
BI518895	BI518895
LOCUS	BI518895
DEFINITION	60301815FL NIH_MGC_118 Homo sapiens cDNA clone IMAGE:511074 5', mRNA sequence.
ACCESSION	BI518895
VERSION	BI518895.1
KEYWORDS	EST.
SOURCE	human
ORGANISM	Homo sapiens
COMMENT	Mammali; Eutheria; Primates; Catarrhini; Hominidae; Homo. Email: gapbs-r@email.nih.gov
REFERENCE	1 ('bases 1 to 739')
AUTHORS	NIH-MGC http://mgc.ncbi.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.
Tissue	Procurement: Life Technologies, Inc.
CDNA	Library Preparation: Life Technologies, Inc.
DNA	Sequencing by: Incyte Genomics, Inc.
Clones	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plates	LLNL1529 row: n column: 03
High quality sequence stop:	738.
Location/Qualifiers	source 1. _r39 /organism="Homo sapiens" /ab_xref="Taxon:9606" /clone="IMAGE:521074" /clone_id="NIH_MGC_118" /tissue_type="leukocyte" /lab_host="DH10B" /note="vector: PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA source: leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range







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 STATE: CA  
 COUNTRY: USA  
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 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/393,985  
 FILING DATE:  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Sholtz, Charles K.  
 REGISTRATION NUMBER: 38,615  
 REFERENCE/DOCKET NUMBER: 8600-0152  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 324-0880  
 TELEFAX: (415) 324-0960  
 INFORMATION FOR SEQ. ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2097, base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: unknown  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI - SENSE: NO  
 ORIGINAL SOURCE:  
 INDIVIDUAL ISOLATE: Rat syntaxin 1A 3' end (en  
 INDIVIDUAL ISOLATE: acids 4-288; GenBank M95734  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 2..859  
 -08-193-985-1

